

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/582,655
Source: IFWP
Date Processed by STIC: 6/22/06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 06/22/2006

PATENT APPLICATION: US/10/582,655

TIME: 12:46:03

Input Set : E:\seqlist.txt

Output Set: N:\CRF4\06222006\J582655.raw

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3 <110> APPLICANT: MIYATA, TOSHIO
4     KUROKAWA, KIYOSHI
5     YAMAMOTO, HIROSHI
6     OKAMOTO, HIROSHI
8 <120> TITLE OF INVENTION: MEGSIN/RAGE/iNOS-OVEREXPRESSING RENAL DISEASE MODEL ANIMALS
9     AND METHODS FOR EVALUATING COMPOUNDS USING THE MODEL ANIMALS
11 <130> FILE REFERENCE: SHIM-019
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/582,655
C--> 13 <141> CURRENT FILING DATE: 2006-06-12
13 <150> PRIOR APPLICATION NUMBER: JP 2003-415779
14 <151> PRIOR FILING DATE: 2003-12-12
16 <160> NUMBER OF SEQ ID NOS: 9
18 <170> SOFTWARE: PatentIn version 3.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 1143
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (1)..(1140)
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33 1          5          10          15
35 aga gag atg gat gac aat caa gga aat gga aat gtg ttc ttt tcc tct      96
36 Arg Glu Met Asp Asp Asn Gln Gly Asn Gly Asn Val Phe Phe Ser Ser
37          20          25          30
39 ctg agc ctc ttc gct gcc ctg gcc ctg gtc cgc ttg ggc gct caa gat      144
40 Leu Ser Leu Phe Ala Ala Leu Ala Leu Val Arg Leu Gly Ala Gln Asp
41          35          40          45
43 gac tcc ctc tct cag att gat aag ttg ctt cat gtt aac act gcc tca      192
44 Asp Ser Leu Ser Gln Ile Asp Lys Leu Leu His Val Asn Thr Ala Ser
45          50          55          60
47 gga tat gga aac tct tct aat agt cag tca ggg ctc cag tct caa ctg      240
48 Gly Tyr Gly Asn Ser Ser Asn Ser Gln Ser Gly Leu Gln Ser Gln Leu
49 65          70          75          80
51 aaa aga gtt ttt tct gat ata aat gca tcc cac aag gat tat gat ctc      288
52 Lys Arg Val Phe Ser Asp Ile Asn Ala Ser His Lys Asp Tyr Asp Leu
53          85          90          95
55 agc att gtg aat ggg ctt ttt gct gaa aaa gtg tat ggc ttt cat aag      336
56 Ser Ile Val Asn Gly Leu Phe Ala Glu Lys Val Tyr Gly Phe His Lys
57          100         105         110
59 gac tac att gag tgt gcc gaa aaa tta tac gat gcc aaa gtg gag cga      384

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61			115					120					125				
63	gtt	gac	ttt	acg	aat	cat	tta	gaa	gac	act	aga	cgt	aat	att	aat	aag	432
64	Val	Asp	Phe	Thr	Asn	His	Leu	Glu	Asp	Thr	Arg	Arg	Asn	Ile	Asn	Lys	
65			130					135					140				
67	tgg	gtt	gaa	aat	gaa	aca	cat	ggc	aaa	atc	aag	aac	gtg	att	ggt	gaa	480
68	Trp	Val	Glu	Asn	Glu	Thr	His	Gly	Lys	Ile	Lys	Asn	Val	Ile	Gly	Glu	
69	145						150				155				160		
71	ggt	ggc	ata	agc	tca	tct	gct	gta	atg	gtg	ctg	gtg	aat	gct	gtg	tac	528
72	Gly	Gly	Ile	Ser	Ser	Ser	Ala	Val	Met	Val	Leu	Val	Asn	Ala	Val	Tyr	
73					165				170						175		
75	ttc	aaa	ggc	aag	tgg	caa	tca	gcc	ttc	acc	aag	agc	gaa	acc	ata	aat	576
76	Phe	Lys	Gly	Lys	Trp	Gln	Ser	Ala	Phe	Thr	Lys	Ser	Glu	Thr	Ile	Asn	
77			180						185				190				
79	tgc	cat	ttc	aaa	tct	ccc	aag	tgc	tct	ggg	aag	gca	gtc	gcc	atg	atg	624
80	Cys	His	Phe	Lys	Ser	Pro	Lys	Cys	Ser	Gly	Lys	Ala	Val	Ala	Met	Met	
81			195					200					205				
83	cat	cag	gaa	cgg	aag	ttc	aat	ttg	tct	gtt	att	gag	gac	cca	tca	atg	672
84	His	Gln	Glu	Arg	Lys	Phe	Asn	Leu	Ser	Val	Ile	Glu	Asp	Pro	Ser	Met	
85			210					215					220				
87	aag	att	ctt	gag	ctc	aga	tac	aat	ggt	ggc	ata	aac	atg	tac	gtt	ctg	720
88	Lys	Ile	Leu	Glu	Leu	Arg	Tyr	Asn	Gly	Gly	Ile	Asn	Met	Tyr	Val	Leu	
89	225					230					235				240		
91	ctg	cct	gag	aat	gac	ctc	tct	gaa	att	gaa	aac	aaa	ctg	acc	ttt	cag	768
92	Leu	Pro	Glu	Asn	Asp	Leu	Ser	Glu	Ile	Glu	Asn	Lys	Leu	Thr	Phe	Gln	
93					245				250						255		
95	aat	cta	atg	gaa	tgg	acc	aat	cca	agg	cga	atg	acc	tct	aag	tat	gtt	816
96	Asn	Leu	Met	Glu	Trp	Thr	Asn	Pro	Arg	Arg	Met	Thr	Ser	Lys	Tyr	Val	
97			260						265					270			
99	gag	gta	ttt	ttt	cct	cag	ttc	aag	ata	gag	aag	aat	tat	gaa	atg	aaa	864
100	Glu	Val	Phe	Phe	Pro	Gln	Phe	Lys	Ile	Glu	Lys	Asn	Tyr	Glu	Met	Lys	
101			275					280					285				
103	caa	tat	ttg	aga	gcc	cta	ggg	ctg	aaa	gat	atc	ttt	gat	gaa	tcc	aaa	912
104	Gln	Tyr	Leu	Arg	Ala	Leu	Gly	Leu	Lys	Asp	Ile	Phe	Asp	Glu	Ser	Lys	
105			290					295					300				
107	gca	gat	ctc	tct	ggg	att	gct	tcg	ggg	ggt	cgt	ctg	tat	ata	tca	agg	960
108	Ala	Asp	Leu	Ser	Gly	Ile	Ala	Ser	Gly	Gly	Arg	Leu	Tyr	Ile	Ser	Arg	
109	305					310					315				320		
111	atg	atg	cac	aaa	tct	tac	ata	gag	gtc	act	gag	gag	ggc	acc	gag	gct	1008
112	Met	Met	His	Lys	Ser	Tyr	Ile	Glu	Val	Thr	Glu	Glu	Gly	Thr	Glu	Ala	
113					325						330				335		
115	act	gct	gcc	aca	gga	agt	aat	att	gta	gaa	aag	caa	ctc	cct	cag	tcc	1056
116	Thr	Ala	Ala	Thr	Gly	Ser	Asn	Ile	Val	Glu	Lys	Gln	Leu	Pro	Gln	Ser	
117			340						345					350			
119	acg	ctg	ttt	aga	gct	gac	cac	cca	ttc	cta	ttt	gtt	atc	agg	aag	gat	1104
120	Thr	Leu	Phe	Arg	Ala	Asp	His	Pro	Phe	Leu	Phe	Val	Ile	Arg	Lys	Asp	
121			355						360					365			
123	gac	atc	atc	tta	ttc	agt	ggc	aaa	gtt	tct	tgc	cct	tga				1143
124	Asp	Ile	Ile	Leu	Phe	Ser	Gly	Lys	Val	Ser	Cys	Pro					

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129 <211> LENGTH: 1391
130 <212> TYPE: DNA
131 <213> ORGANISM: Homo sapiens
133 <220> FEATURE:
134 <221> NAME/KEY: CDS
135 <222> LOCATION: (1)..(1215)
138 <400> SEQUENCE: 2
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140 Gly Ala Ala Gly Thr Ala Val Gly Ala Trp Val Leu Val Leu Ser Leu
141 1      5      10      15
143 tgg ggg gca gta gta ggt gct caa aac atc aca gcc cgg att ggc gag      96
144 Trp Gly Ala Val Gly Ala Gln Asn Ile Thr Ala Arg Ile Gly Glu
145      20      25      30
147 cca ctg gtg ctg aag tgt aag ggg gcc ccc aag aaa cca ccc cag cgg      144
148 Pro Leu Val Leu Lys Cys Lys Gly Ala Pro Lys Lys Pro Pro Gln Arg
149      35      40      45
151 ctg gaa tgg aaa ctg aac aca ggc cgg aca gaa gct tgg aag gtc ctg      192
152 Leu Glu Trp Lys Leu Asn Thr Gly Arg Thr Glu Ala Trp Lys Val Leu
153      50      55      60
155 tct ccc cag gga gga ggc ccc tgg gac agt gtg gct cgt gtc ctt ccc      240
156 Ser Pro Gln Gly Gly Gly Pro Trp Asp Ser Val Ala Arg Val Leu Pro
157 65      70      75      80
159 aac ggc tcc ctc ttc ctt ccg gct gtc ggg atc cag gat gag ggg att      288
160 Asn Gly Ser Leu Phe Leu Pro Ala Val Gly Ile Gln Asp Glu Gly Ile
161      85      90      95
163 ttc cgg tgc agg gca atg aac agg aat gga aag gag acc aag tcc aac      336
164 Phe Arg Cys Arg Ala Met Asn Arg Asn Gly Lys Glu Thr Lys Ser Asn
165      100      105      110
167 tac cga gtc cgt gtc tac cag att cct ggg aag cca gaa att gta gat      384
168 Tyr Arg Val Arg Val Tyr Gln Ile Pro Gly Lys Pro Glu Ile Val Asp
169      115      120      125
171 tct gcc tct gaa ctc acg gct ggt gtt ccc aat aag gtg ggg aca tgt      432
172 Ser Ala Ser Glu Leu Thr Ala Gly Val Pro Asn Lys Val Gly Thr Cys
173      130      135      140
175 gtg tca gag gga agc tac cct gca ggg act ctt agc tgg cac ttg gat      480
176 Val Ser Glu Gly Ser Tyr Pro Ala Gly Thr Leu Ser Trp His Leu Asp
177 145      150      155      160
179 ggg aag ccc ctg gtg cct aat gag aag gga gta tct gtg aag gaa cag      528
180 Gly Lys Pro Leu Val Pro Asn Glu Lys Gly Val Ser Val Lys Glu Gln
181      165      170      175
183 acc agg aga cac cct gag aca ggg ctc ttc aca ctg cag tcg gag cta      576
184 Thr Arg Arg His Pro Glu Thr Gly Leu Phe Thr Leu Gln Ser Glu Leu
185      180      185      190
187 atg gtg acc cca gcc cgg gga gga gat ccc cgt ccc acc ttc tcc tgt      624
188 Met Val Thr Pro Ala Arg Gly Gly Asp Pro Arg Pro Thr Phe Ser Cys
189      195      200      205
191 agc ttc agc cca ggc ctt ccc cga cac cgg gcc ttg cgc aca gcc ccc      672

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192 Ser Phe Ser Pro Gly Leu Pro Arg His Arg Ala Leu Arg Thr Ala Pro
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196 Ile Gln Pro Arg Val Trp Glu Pro Val Pro Leu Glu Glu Val Gln Leu
197 225      230      235      240
199 gtg gtg gag cca gaa ggt gga gca gta gct cct ggt gga acc gta acc      768
200 Val Val Glu Pro Glu Gly Gly Ala Val Ala Pro Gly Gly Thr Val Thr
201      245      250      255
203 ctg acc tgt gaa gtc cct gcc cag ccc tct cct caa atc cac tgg atg      816
204 Leu Thr Cys Glu Val Pro Ala Gln Pro Ser Pro Gln Ile His Trp Met
205      260      265      270
207 aag gat ggt gtg ccc ttg ccc ctt ccc ccc agc cct gtg ctg atc ctc      864
208 Lys Asp Gly Val Pro Leu Pro Leu Pro Pro Ser Pro Val Leu Ile Leu
209      275      280      285
211 cct gag ata ggg cct cag gac cag gga acc tac agc tgt gtg gcc acc      912
212 Pro Glu Ile Gly Pro Gln Asp Gln Gly Thr Tyr Ser Cys Val Ala Thr
213      290      295      300
215 cat tcc agc cac ggg ccc cag gaa agc cgt gct gtc agc atc agc atc      960
216 His Ser Ser His Gly Pro Gln Glu Ser Arg Ala Val Ser Ile Ser Ile
217 305      310      315      320
219 atc gaa cca ggc gag gag ggg cca act gca ggc tct gtg gga gga tca      1008
220 Ile Glu Pro Gly Glu Glu Gly Pro Thr Ala Gly Ser Val Gly Gly Ser
221      325      330      335
223 ggg ctg gga act cta gcc ctg gcc ctg ggg atc ctg gga ggc ctg ggg      1056
224 Gly Leu Gly Thr Leu Ala Leu Ala Leu Gly Ile Leu Gly Gly Leu Gly
225      340      345      350
227 aca gcc gcc ctg ctc att ggg gtc atc ttg tgg caa agg cgg caa cgc      1104
228 Thr Ala Ala Leu Leu Ile Gly Val Ile Leu Trp Gln Arg Arg Gln Arg
229      355      360      365
231 cga gga gag gag agg aag gcc cca gaa aac cag gag gaa gag gag gag      1152
232 Arg Gly Glu Glu Arg Lys Ala Pro Glu Asn Gln Glu Glu Glu Glu Glu
233      370      375      380
235 cgt gca gaa ctg aat cag tcg gag gaa cct gag gca ggc gag agt agt      1200
236 Arg Ala Glu Leu Asn Gln Ser Glu Glu Pro Glu Ala Gly Glu Ser Ser
237 385      390      395      400
239 act gga ggg cct tga gggggccaca gacagatccc atccatcagc tcccttttct      1255
240 Thr Gly Gly Pro
243 ttttcccttg aactgttctg gcctcagacc aactctctcc tgtataatct ctctcctgta      1315
245 taacccccacc ttgccaaagt ttcttctaca accagagccc cccacaatga tgattaaaca      1375
247 cctgacacat cttgca      1391
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251 <211> LENGTH: 3991
252 <212> TYPE: DNA
253 <213> ORGANISM: Mus musculus
255 <220> FEATURE:
256 <221> NAME/KEY: CDS
257 <222> LOCATION: (185)..(3619)
260 <400> SEQUENCE: 3
261 agggcccccag ggacacagtg tcaactggttt gaaacttctc agccaccttg gtgaaggagc      60

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263	tgagctgtta	gagacacttc	tgaggctcct	cacgcttggg	tcttggttcac	tccacggagt	120
265	agcctagtca	actgcaagag	aacggagaaac	gttggatttg	gagcagaagt	gcaaagtctc	180
267	agac atg gct tgc ccc tgg aag ttt ctc ttc aaa gtc aaa tcc tac caa	229					
268	Met Ala Cys Pro Trp Lys Phe Leu Phe Lys Val Lys Ser Tyr Gln						
269	1 5 10 15						
271	agt gac ctg aaa gag gaa aag gac att aac aac aac gtg aag aaa acc	277					
272	Ser Asp Leu Lys Glu Glu Lys Asp Ile Asn Asn Asn Val Lys Lys Thr						
273	20 25 30						
275	cct tgt gct gtt ctc agc cca aca ata caa gat gac cct aag agt cac	325					
276	Pro Cys Ala Val Leu Ser Pro Thr Ile Gln Asp Asp Pro Lys Ser His						
277	35 40 45						
279	caa aat ggc tcc ccg cag ctc ctc act ggg aca gca cag aat gtt cca	373					
280	Gln Asn Gly Ser Pro Gln Leu Leu Thr Gly Thr Ala Gln Asn Val Pro						
281	50 55 60						
283	gaa tcc ctg gac aag ctg cat gtg aca tgc acc cgt cca cag tat gtg	421					
284	Glu Ser Leu Asp Lys Leu His Val Thr Ser Thr Arg Pro Gln Tyr Val						
285	65 70 75						
287	agg atc aaa aac tgg ggc agt gga gag att ttg cat gac act ctt cac	469					
288	Arg Ile Lys Asn Trp Gly Ser Gly Glu Ile Leu His Asp Thr Leu His						
289	80 85 90 95						
291	cac aag gcc aca tgc gat ttc act tgc aag tcc aag tct tgc ttg ggg	517					
292	His Lys Ala Thr Ser Asp Phe Thr Cys Lys Ser Lys Ser Cys Leu Gly						
293	100 105 110						
295	tcc atc atg aac ccc aag agt ttg acc aga gga ccc aga gac aag cct	565					
296	Ser Ile Met Asn Pro Lys Ser Leu Thr Arg Gly Pro Arg Asp Lys Pro						
297	115 120 125						
299	acc cct ctg gag gag ctc ctg cct cat gcc att gag ttc atc aac cag	613					
300	Thr Pro Leu Glu Glu Leu Leu Pro His Ala Ile Glu Phe Ile Asn Gln						
301	130 135 140						
303	tat tat ggc tcc ttt aaa gag gca aaa ata gag gaa cat ctg gcc agg	661					
304	Tyr Tyr Gly Ser Phe Lys Glu Ala Lys Ile Glu Glu His Leu Ala Arg						
305	145 150 155						
307	ctg gaa gct gta aca aag gaa ata gaa aca aca gga acc tac cag ctc	709					
308	Leu Glu Ala Val Thr Lys Glu Ile Glu Thr Thr Gly Thr Tyr Gln Leu						
309	160 165 170 175						
311	act ctg gat gag ctc atc ttt gcc acc aag atg gcc tgg agg aat gcc	757					
312	Thr Leu Asp Glu Leu Ile Phe Ala Thr Lys Met Ala Trp Arg Asn Ala						
313	180 185 190						
315	cct cgc tgc atc ggc agg atc cag tgg tcc aac ctg cag gtc ttt gac	805					
316	Pro Arg Cys Ile Gly Arg Ile Gln Trp Ser Asn Leu Gln Val Phe Asp						
317	195 200 205						
319	gct cgg aac tgt agc aca gca cag gaa atg ttt cag cac atc tgc aga	853					
320	Ala Arg Asn Cys Ser Thr Ala Gln Glu Met Phe Gln His Ile Cys Arg						
321	210 215 220						
323	cac ata ctt tat gcc acc aac aat ggc aac atc agg tgc gcc atc act	901					
324	His Ile Leu Tyr Ala Thr Asn Asn Gly Asn Ile Arg Ser Ala Ile Thr						
325	225 230 235						
327	gtg ttc ccc cag cgg agt gac ggc aaa cat gac ttc agg ctc tgg aat	949					
328	Val Phe Pro Gln Arg Ser Asp Gly Lys His Asp Phe Arg Leu Trp Asn						

RAW SEQUENCE LISTING ERROR SUMMARY
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:4,5,6,7,8,9

VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date